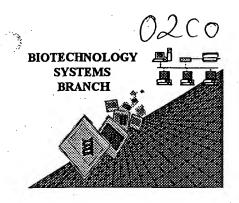BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: *09/468,149*

Art Unit / Team No. : *0 1 P E*

Date Processed by STIC: *1/13/2000*

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>   <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/468,147_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

niH
5-11-W
#4

┌───┐
│   This Raw Listing contains the General   │
│   Information Section and those Sequences   │
│   containing ERRORS.   │
└───┘

Does Not Comply
Corrected Diskette Needed

     1   <110> Schlauder, George G
     2   Erker, James C
     3   Desai, Suresh M
     4   Dawson, George J
     5   Mushawar, Isa K   *pp 10-12*
     6   <120> METHODS AND COMPOSITIONS FOR DETECTING HEPATITIS E
     7   VIRUS
     8   <130> 6232.US.01
     9   <140> US/09/468,147
    10   <141> 1999-12-21
    11   <150> US 09/173,141
    12   <151> 1998-10-15
    13   <160> 258
    14   <170> PatentIn Ver. 2.0

ERRORED SEQUENCES FOLLOW

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    15   <210> 90
    16   <211> 7202
    17   <212> DNA
    18   <213> Hepatitis E virus   *see*
    19   <220>
    20   <221> CDS   *P 10*
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    26   <223> orf2
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    29   <222> ()..)
    30   <223> CDS- orf3
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    32   <223> us1full
    33   <400> 90
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    35   Pro Gly Ile Thr Thr Ala Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn
    36   1   5   10   15
    37   tct gcc ttg gcg aat gct gtg gtg gtt cgg ccg ttt tta tct cgc gtg   96
    38   Ser Ala Leu Ala Asn Ala Val Val Val Arg Pro Phe Leu Ser Arg Val
    39   20   25   30

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40    caa acc gag att ctt att aat ttg atg caa ccc cgg cag ttg gtt ttc    144
41    Gln Thr Glu Ile Leu Ile Asn Leu Met Gln Pro Arg Gln Leu Val Phe
42             35                  40                  45
43    cgc cct gag gta ctt tgg aat cac cct atc cag cgg gtt ata cat aat    192
44    Arg Pro Glu Val Leu Trp Asn His Pro Ile Gln Arg Val Ile His Asn
45             50                  55                  60
46    gaa tta gaa cag tac tgc cgg gct cgg gct ggt cgt tgc ttg gag gtt    240
47    Glu Leu Glu Gln Tyr Cys Arg Ala Arg Ala Gly Arg Cys Leu Glu Val
48    65                  70                  75                  80
49    gga gct cac cca aga tcc att aat gac aac ccc aac gtt ctg cat cgg    288
50    Gly Ala His Pro Arg Ser Ile Asn Asp Asn Pro Asn Val Leu His Arg
51                      85                  90                  95
52    tgt ttc ctt aga ccg gtt ggc cga gat gtt cag cgc tgg tac tct gcc    336
53    Cys Phe Leu Arg Pro Val Gly Arg Asp Val Gln Arg Trp Tyr Ser Ala
54             100                 105                 110
55    ccc acc cgc ggc cct gcg gct aat tgc cgc cgc tcc gcg ttg cgt ggt    384
56    Pro Thr Arg Gly Pro Ala Ala Asn Cys Arg Arg Ser Ala Leu Arg Gly
57             115                 120                 125
58    ctc ccc ccc gct gac cgc act tac tgc ttt gat gga ttc tcc cgt tgt    432
59    Leu Pro Pro Ala Asp Arg Thr Tyr Cys Phe Asp Gly Phe Ser Arg Cys
60             130                 135                 140
61    gct ttt gct gca gag acc ggt gtg gct ctt tac tct ctg cat gac ctt    480
62    Ala Phe Ala Ala Glu Thr Gly Val Ala Leu Tyr Ser Leu His Asp Leu
63    145                 150                 155                 160
64    tgg cca gct gat gtt gca gag gct atg gcc cgc cac ggg atr aca cgc    528
65    Trp Pro Ala Asp Val Ala Glu Ala Met Ala Arg His Gly Xaa Thr Arg
66                      165                 170                 175
67    ttg tat gcc gca ctg cac ctt ccc cct gag gtg ctg cta cca ccc ggc    576
68    Leu Tyr Ala Ala Leu His Leu Pro Pro Glu Val Leu Leu Pro Pro Gly
69             180                 185                 190
70    acc tac cac aca acc tcg tat ctc ctg att cac gac ggc gac cgc gct    624
71    Thr Tyr His Thr Thr Ser Tyr Leu Leu Ile His Asp Gly Asp Arg Ala
72             195                 200                 205
73    gtt gta act tac gag ggc gat act agt gcg ggc tat aat cat gat gtc    672
74    Val Val Thr Tyr Glu Gly Asp Thr Ser Ala Gly Tyr Asn His Asp Val
75             210                 215                 220
76    tcc ata ctt cgt gcg tgg atc cgt act aca aaa ata gtt ggt gat cat    720
77    Ser Ile Leu Arg Ala Trp Ile Arg Thr Thr Lys Ile Val Gly Asp His
78    225                 230                 235                 240
79    ccg ttg gtc ata gag cgt gtg cgg gcc att gga tgt cat ttt gtg ttg    768
80    Pro Leu Val Ile Glu Arg Val Arg Ala Ile Gly Cys His Phe Val Leu
81                      245                 250                 255
82    ctg ctc acc gca gcc cct gag ccg tca ccc atg cct tat gtt cct tac    816
83    Leu Leu Thr Ala Ala Pro Glu Pro Ser Pro Met Pro Tyr Val Pro Tyr
84             260                 265                 270
85    cct cgt tca acg gag gtg tat gtc cgg tcc ata ttt ggc cct ggc ggc    864
86    Pro Arg Ser Thr Glu Val Tyr Val Arg Ser Ile Phe Gly Pro Gly Gly
87             275                 280                 285
88    tcc cca tcc ttg ttt ccg tca gcc tgc tct act aaa tct act ttc cat    912
89    Ser Pro Ser Leu Phe Pro Ser Ala Cys Ser Thr Lys Ser Thr Phe His
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OIPE

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 91      gct gtc ccg gtg cat atc tgg gat cgg ctc atg ctc ttt ggt gcc acc      960
 92      Ala Val Pro Val His Ile Trp Asp Arg Leu Met Leu Phe Gly Ala Thr
 93      305              310              315              320
 94      ctg gac gat cag gcg ttt tgc tgt tca cgg ctc atg act tac ctc cgt     1008
 95      Leu Asp Asp Gln Ala Phe Cys Cys Ser Arg Leu Met Thr Tyr Leu Arg
 96                       325              330              335
 97      ggt att agt tac aag gtc act gtc ggc gcg ctt gtc gct aat gag ggg     1056
 98      Gly Ile Ser Tyr Lys Val Thr Val Gly Ala Leu Val Ala Asn Glu Gly
 99                       340              345              350
100      tgg aac gcc tct gaa gac gct ctt act gca rtg atc act gca gct tat     1104
101      Trp Asn Ala Ser Glu Asp Ala Leu Thr Ala Xaa Ile Thr Ala Ala Tyr
102                  355              360              365
103      ttg act att tgc cat cag cgt tat ctc cgc acc cag gcg ata tcc aag     1152
104      Leu Thr Ile Cys His Gln Arg Tyr Leu Arg Thr Gln Ala Ile Ser Lys
105          370              375              380
106      ggc atg cgc cgg ttg ggg gtt gag cac gcc cag aaa ttt atc aca aga     1200
107      Gly Met Arg Arg Leu Gly Val Glu His Ala Gln Lys Phe Ile Thr Arg
108      385              390              395              400
109      ctc tac agt tgg cta ttt gag aag tct ggc cgt gat tat atc ccc ggc     1248
110      Leu Tyr Ser Trp Leu Phe Glu Lys Ser Gly Arg Asp Tyr Ile Pro Gly
111                       405              410              415
112      cgc cag ctt cag ttc tat gca cag tgc cga cgg tgg cta tct gca ggc     1296
113      Arg Gln Leu Gln Phe Tyr Ala Gln Cys Arg Arg Trp Leu Ser Ala Gly
114                  420              425              430
115      ttc cac cta gac ccc agg gta ctt gtt ttt gat gag tca gta cca tgc     1344
116      Phe His Leu Asp Pro Arg Val Leu Val Phe Asp Glu Ser Val Pro Cys
117              435              440              445
118      cgc tgt agg acg ttt ttg aag aaa gtt gcg ggt aaa ttc tgc tgt ttt     1392
119      Arg Cys Arg Thr Phe Leu Lys Lys Val Ala Gly Lys Phe Cys Cys Phe
120          450              455              460
121      atg cgg tgg ctc ggg cag gag tgt acc tgc ttc ttg gag ccg gcc gag     1440
122      Met Arg Trp Leu Gly Gln Glu Cys Thr Cys Phe Leu Glu Pro Ala Glu
123      465              470              475              480
124      ggt tta gtc ggc gat cat ggc cat gac aac gag gcc tat gag ggt tct     1488
125      Gly Leu Val Gly Asp His Gly His Asp Asn Glu Ala Tyr Glu Gly Ser
126                  485              490              495
127      gag gtc gac ccg gct gaa cct gca cat ctt gat gtt tct ggg act tac     1536
128      Glu Val Asp Pro Ala Glu Pro Ala His Leu Asp Val Ser Gly Thr Tyr
129              500              505              510
130      gcc gtc cac ggg cac cag ctt gag gcc ctc tat agg gca ctt aat gtc     1584
131      Ala Val His Gly His Gln Leu Glu Ala Leu Tyr Arg Ala Leu Asn Val
132          515              520              525
133      cca caa gat att gcc gct cga gct tcc cga cta acg gca act gtt gag     1632
134      Pro Gln Asp Ile Ala Ala Arg Ala Ser Arg Leu Thr Ala Thr Val Glu
135          530              535              540
136      ctc gtt gca agt cca gac cgc tta gag tgc cgc acc gtg ctc ggt aat     1680
137      Leu Val Ala Ser Pro Asp Arg Leu Glu Cys Arg Thr Val Leu Gly Asn
138      545              550              555              560
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143        Gly Pro Glu Gln Tyr Val Leu Ser Phe Asp Ala Ser Arg Gln Ser Met
144                        580                 585                 590
145        ggg gcc ggg tcg cat agc ctc act tat gag ctc acc cct gct ggt ttg    1824
146        Gly Ala Gly Ser His Ser Leu Thr Tyr Glu Leu Thr Pro Ala Gly Leu
147                        595                 600                 605
148        cag gtt agg att tca tct aat ggt ctg gat tgc act gct aca ttc ccc    1872
149        Gln Val Arg Ile Ser Ser Asn Gly Leu Asp Cys Thr Ala Thr Phe Pro
150            610                     615                 620
151        ccc ggt gga gcc cct agc gct gcg ccc ggg gag gtg gca gcc ttt tgc    1920
152        Pro Gly Gly Ala Pro Ser Ala Ala Pro Gly Glu Val Ala Ala Phe Cys
153        625                     630                 635                 640
154        agt gcc ctt tat aga tat aac agg ttc acc cag cgg cac tcg ctg act    1968
155        Ser Ala Leu Tyr Arg Tyr Asn Arg Phe Thr Gln Arg His Ser Leu Thr
156                        645                 650                 655
157        ggc gga tta tgg tta cac cct gag ggg ttg ctg ggt att ttc ccc cct    2016
158        Gly Gly Leu Trp Leu His Pro Glu Gly Leu Leu Gly Ile Phe Pro Pro
159                        660                 665                 670
160        ttc tcc cct ggg cat atc tgg gag tct gcg aac ccc ttt tgc ggg gag    2064
161        Phe Ser Pro Gly His Ile Trp Glu Ser Ala Asn Pro Phe Cys Gly Glu
162                        675                 680                 685
163        ggg act ttg tat acc cga act tgg tca aca tct ggc ttt tct agt gat    2112
164        Gly Thr Leu Tyr Thr Arg Thr Trp Ser Thr Ser Gly Phe Ser Ser Asp
165            690                     695                 700
166        ttc tcc ccc cct gaa gcg gcc gct cct gct atg gct gct acc ccg ggg    2160
167        Phe Ser Pro Pro Glu Ala Ala Ala Pro Ala Met Ala Ala Thr Pro Gly
168        705                     710                 715                 720
169        ctg ccc cat tct acc cca cct gtt agc gat att tgg gtg cta cca ccg    2208
170        Leu Pro His Ser Thr Pro Pro Val Ser Asp Ile Trp Val Leu Pro Pro
171                        725                 730                 735
172        ccc tca gag gag ttt cag gtt gat gca gca cct gtg ccc cct gcc cct    2256
173        Pro Ser Glu Glu Phe Gln Val Asp Ala Ala Pro Val Pro Pro Ala Pro
174                        740                 745                 750
175        gac cct gct gga ttg ccc ggt ccc gtt gtg ctt acc ccc ccc ccc cct    2304
176        Asp Pro Ala Gly Leu Pro Gly Pro Val Val Leu Thr Pro Pro Pro Pro
177                        755                 760                 765
178        ccc cct gtg cat aag cca tca ata ccc ccg cct tcc cgt aac cgt cgt    2352
179        Pro Pro Val His Lys Pro Ser Ile Pro Pro Pro Ser Arg Asn Arg Arg
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182        Leu Leu Tyr Thr Tyr Pro Asp Gly Ala Lys Val Tyr Ala Gly Ser Leu
183        785                     790                 795                 800
184        ttt gaa tca gac tgt gac tgg ctg gtt aat gcc tca aac ccg ggc cat    2448
185        Phe Glu Ser Asp Cys Asp Trp Leu Val Asn Ala Ser Asn Pro Gly His
186                        805                 810                 815
187        cgt ccc gga ggt ggc ctc tgc cat gcc ttt tac caa cgt ttt cca gaa    2496
188        Arg Pro Gly Gly Gly Leu Cys His Ala Phe Tyr Gln Arg Phe Pro Glu
189                        820                 825                 830
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190	gcg ttt tac cca act gaa ttc atc atg cgt gag ggt ctt gca gca tac	2544
191	Ala Phe Tyr Pro Thr Glu Phe Ile Met Arg Glu Gly Leu Ala Ala Tyr	
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193	acc ttg acc ccg cgc cct atc att cat gca gtc gct ccc gat tat agg	2592
194	Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala Pro Asp Tyr Arg	
195	850 855 860	
196	gtt gag cag aac ccg aag agg ctt gag gca gcg tac cgt gaa act tgt	2640
197	Val Glu Gln Asn Pro Lys Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys	
198	865 870 875 880	
199	tcc cgt cgt ggc acc gct gcc tac ccg ctt ttg ggt tcg ggt ata tac	2688
200	Ser Arg Arg Gly Thr Ala Ala Tyr Pro Leu Leu Gly Ser Gly Ile Tyr	
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202	cag gtc cct gtt agc ctc agt ttt gat gcc tgg gaa cgt aat cac cgc	2736
203	Gln Val Pro Val Ser Leu Ser Phe Asp Ala Trp Glu Arg Asn His Arg	
204	900 905 910	
205	ccc ggc gat gag ctt tac ttg acc gag ccc gct gca aat tgg ttt gag	2784
206	Pro Gly Asp Glu Leu Tyr Leu Thr Glu Pro Ala Ala Asn Trp Phe Glu	
207	915 920 925	
208	gct aat aag ccg gcg cag ccg gtg ctc acc ata act gag gac acg gcc	2832
209	Ala Asn Lys Pro Ala Gln Pro Val Leu Thr Ile Thr Glu Asp Thr Ala	
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211	cgt acg gcc aac ctg gca ttg gag att gat gcc gct aca gag gtc ggc	2880
212	Arg Thr Ala Asn Leu Ala Leu Glu Ile Asp Ala Ala Thr Glu Val Gly	
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215	Arg Ala Cys Ala Gly Cys Thr Ile Ser Pro Gly Ile Val His Tyr Gln	
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223	tgg cgc cgc cgg ggt ttt gcg gcc ttc aca ccc cac aca gcg gcc cgt	3072
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225	1010 1015 1020	
226	gtt act atc ggc cgc cgc gtt gtg att gat gag gct cca tct ctc ccg	3120
227	Val Thr Ile Gly Arg Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro	
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230	Pro His Leu Leu Leu Leu His Met Gln Arg Ala Ser Ser Val His Leu	
231	1045 1050 1055	
232	ctc ggt gac cca aat cag atc cct gct att gat ttt gag cac gcc ggc	3216
233	Leu Gly Asp Pro Asn Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly	
234	1060 1065 1070	
235	ctg gtc cct gcg atc cgt ccc gag ctt gcg cca acg agc tgg tgg crc	3264
236	Leu Val Pro Ala Ile Arg Pro Glu Leu Ala Pro Thr Ser Trp Trp Xaa	
237	1075 1080 1085	
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244     aat gaa ccg gcc att ggc cag aag ttg gtt ytc acg cag gcg gca aag    3408
245     Asn Glu Pro Ala Ile Gly Gln Lys Leu Val Xaa Thr Gln Ala Ala Lys
246                  1125          1130              1135
247     gct gct aac cct ggt gcg att acg gtc cac gaa gct cag ggt gcc acc    3456
248     Ala Ala Asn Pro Gly Ala Ile Thr Val His Glu Ala Gln Gly Ala Thr
249                  1140          1145              1150
250     ttc aca gag acc aca atc ata gcc acg gcc gac gcc agg ggc ctt atc    3504
251     Phe Thr Glu Thr Thr Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile
252            1155            1160              1165
253     cag tca tcc cgg gct cat gct ata gtt gca ctt act cgc cac act gag    3552
254     Gln Ser Ser Arg Ala His Ala Ile Val Ala Leu Thr Arg His Thr Glu
255            1170            1175              1180
256     aag tgt gtt atc ctg gat gcc ccc ggc ctg ctt cgt gag gtc ggc att    3600
257     Lys Cys Val Ile Leu Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile
258     1185            1190            1195              1200
259     tcg gat gtg att gtc aac aac ttt ttc ctt gct ggt ggc gag gtc ggc    3648
260     Ser Asp Val Ile Val Asn Asn Phe Phe Leu Ala Gly Gly Glu Val Gly
261                  1205            1210              1215
262     crc cac cgc cct tct gtg ata cct cgc ggt aac cct gat caa aac ctc    3696
263     Xaa His Arg Pro Ser Val Ile Pro Arg Gly Asn Pro Asp Gln Asn Leu
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265     ggg act tta cag gcc ttc ccg ccg tcc tgt caa att agt gct tac cat    3744
266     Gly Thr Leu Gln Ala Phe Pro Pro Ser Cys Gln Ile Ser Ala Tyr His
267            1235            1240              1245
268     cag ttg gct gag gaa ctg ggc cat cgc ccg gcc cct gtc gcc gcc gtc    3792
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271     ttg ccc cct tgc cct gag ctt gag cag ggc ctg ctc tac atg cca cag    3840
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274     gag ctc act gtg tcc gat agt gtg ttg gtt ttt gag ctt acg gat ata    3888
275     Glu Leu Thr Val Ser Asp Ser Val Leu Val Phe Glu Leu Thr Asp Ile
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282            1315            1320              1325
283     cat tca gat gtt cgt gag tcc cta gct agg ttc atc cct act atc ggg    4032
284     His Ser Asp Val Arg Glu Ser Leu Ala Arg Phe Ile Pro Thr Ile Gly
285            1330            1335              1340
286     cct gtt cag gct acc aca tgt gag ttg tat gag ttg gtt gag gct atg    4080
287     Pro Val Gln Ala Thr Thr Cys Glu Leu Tyr Glu Leu Val Glu Ala Met
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293        Asn Arg Asp Val Ser Arg Ile Thr Phe Phe Gln Lys Xaa Cys Asn Lys
294                 1380                1385                1390
295        ttt aca act ggt gag acc atc gcc cac ggc aag gtt ggc cag ggt ata   4224
296        Phe Thr Thr Gly Glu Thr Ile Ala His Gly Lys Val Gly Gln Gly Ile
297                 1395                1400                1405
298        tcg gcc tgg agt aag acc ttc tgc gct ctg ttc ggc ccg tgg ttc cgc   4272
299        Ser Ala Trp Ser Lys Thr Phe Cys Ala Leu Phe Gly Pro Trp Phe Arg
300                 1410                1415                1420
301        gcc att gaa aaa gaa ata ttg gcc ctg ctc ccg cct aat atc ttt tat   4320
302        Ala Ile Glu Lys Glu Ile Leu Ala Leu Leu Pro Pro Asn Ile Phe Tyr
303             1425                1430                1435                1440
304        ggc gac gct tat gag gag tca gtt ttt gcc gcc gct gtg tcc ggg gcg   4368
305        Gly Asp Ala Tyr Glu Glu Ser Val Phe Ala Ala Ala Val Ser Gly Ala
306                 1445                1450                1455
307        ggg tca tgt atg gta ttt gaa aat gac ttt tca gag ttt gac agt acc   4416
308        Gly Ser Cys Met Val Phe Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr
309                 1460                1465                1470
310        cag aat aat ttc tct ctt ggc ctt gag tgt gtg gtt atg gag gag tgc   4464
311        Gln Asn Asn Phe Ser Leu Gly Leu Glu Cys Val Val Met Glu Glu Cys
312                 1475                1480                1485
313        ggc atg cct caa tgg cta att agg ttg tac cat ctg gtt cgg tct gcc   4512
314        Gly Met Pro Gln Trp Leu Ile Arg Leu Tyr His Leu Val Arg Ser Ala
315             1490                1495                1500
316        tgg att ctg cag gcg ccg aag gag tct ctt aag ggt ttc tgg aag aag   4560
317        Trp Ile Leu Gln Ala Pro Lys Glu Ser Leu Lys Gly Phe Trp Lys Lys
318        1505                1510                1515                1520
319        cat tct ggt gag cct ggt acc ctt ctt tgg aat acc gtc tgg aat atg   4608
320        His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn Met
321                 1525                1530                1535
322        gcg att ata gca cat tgc tat gag ttc cgt gac ttt cgt gtt gct gcc   4656
323        Ala Ile Ile Ala His Cys Tyr Glu Phe Arg Asp Phe Arg Val Ala Ala
324             1540                1545                1550
325        ttt aag ggt gat gat tcg gtg gtc ctc tgt agt gac tac cga cag agc   4704
326        Phe Lys Gly Asp Asp Ser Val Val Leu Cys Ser Asp Tyr Arg Gln Ser
327             1555                1560                1565
328        cgc aat gca gct gcc tta att gct ggc tgt ggg ctc aaa ttg aag gtt   4752
329        Arg Asn Ala Ala Ala Leu Ile Ala Gly Cys Gly Leu Lys Leu Lys Val
330             1570                1575                1580
331        gat tac cgc cct atc ggg ctg tat gct ggg gtg gtg gtg gcc ccc ggt   4800
332        Asp Tyr Arg Pro Ile Gly Leu Tyr Ala Gly Val Val Val Ala Pro Gly
333        1585                1590                1595                1600
334        ttg ggg aca ctg ccc gat gtg gtg cgt ttt gct ggt cgg ttg tct gaa   4848
335        Leu Gly Thr Leu Pro Asp Val Val Arg Phe Ala Gly Arg Leu Ser Glu
336                 1605                1610                1615
337        aag aat tgg ggc ccc ggc ccg gaa cgt gct gag cag ctg cgt ctt gct   4896
338        Lys Asn Trp Gly Pro Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala
339                 1620                1625                1630
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340    gtc tgc gac ttc ctt cga ggg ttg acg aat gtt gcg cag gtc tgt gtt   4944
341    Val Cys Asp Phe Leu Arg Gly Leu Thr Asn Val Ala Gln Val Cys Val
342           1635              1640              1645
343    gat gtt gtg tcc cgt gtc tat gga gtc agc ccc ggg ctc gta cat aac   4992
344    Asp Val Val Ser Arg Val Tyr Gly Val Ser Pro Gly Leu Val His Asn
345       1650              1655              1660
346    ctt att ggc atg ctg cag acc atc gcc gat ggc aag gcc cac ttt aca   5040
347    Leu Ile Gly Met Leu Gln Thr Ile Ala Asp Gly Lys Ala His Phe Thr
348       1665              1670              1675              1680
349    gag act att aaa cct gta ctt gat ctc aca aat tcc atc ata cag cgg   5088
350    Glu Thr Ile Lys Pro Val Leu Asp Leu Thr Asn Ser Ile Ile Gln Arg
351           1685              1690              1695
352    gtg gaa tga ataacatgtc ttttgcatcg cccatgggat cacc atg cgc cct agg 5143
353    Val Glu                                          Met Arg Pro Arg
354                                                        1700
355    gct gtt ctg ttg ttg ttc ctc atg ttt ctg cct atg ctg ccc gcg cca   5191
356    Ala Val Leu Leu Leu Phe Leu Met Phe Leu Pro Met Leu Pro Ala Pro
357           1705              1710              1715
358    ccg gcc ggt cag ccg tct ggc cgt cgc cgt ggg cgg cgc agc ggc ggt   5239
359    Pro Ala Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg Arg Ser Gly Gly
360    1720              1725              1730              1735
361    gcc ggc ggt ggt ttc tgg agt gac agg gtt gat tct cag ccc ttc gcc   5287
362    Ala Gly Gly Gly Phe Trp Ser Asp Arg Val Asp Ser Gln Pro Phe Ala
363               1740              1745              1750
364    ctc ccc tat att cat cca acc aac ccc ttc gcc gcc gat gtc gtt tca   5335
365    Leu Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Ala Asp Val Val Ser
366           1755              1760              1765
367    caa ccc ggg gct gga act cgc cct cga cag ccg ccc cgc ccc ctc ggt   5383
368    Gln Pro Gly Ala Gly Thr Arg Pro Arg Gln Pro Pro Arg Pro Leu Gly
369           1770              1775              1780
370    tcc gct tgg cgt gac cag tcc aag cgc ccc tcc gtt gcc ccc cgt cgt   5431
371    Ser Ala Trp Arg Asp Gln Ser Lys Arg Pro Ser Val Ala Pro Arg Arg
372       1785              1790              1795
373    cga tct acc cca gct ggg gct gcg ccg cta act gcc ata tca cca gcc   5479
374    Arg Ser Thr Pro Ala Gly Ala Ala Pro Leu Thr Ala Ile Ser Pro Ala
375    1800              1805              1810              1815
376    cct gat aca gct cct gta cct gat gtt gac tca cgt ggt gct att ttg   5527
377    Pro Asp Thr Ala Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu
378               1820              1825              1830
379    cgc cgg cag tac aat ttg tct acg tcc ccg ctt aca tca tct gtt gct   5575
380    Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr Ser Ser Val Ala
381           1835              1840              1845
382    tct ggt act aat ctg gtt ctc tat gct gcc ccg ctg aac cct ctc ttg   5623
383    Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu Asn Pro Leu Leu
384           1850              1855              1860
385    cct ctt cag gat ggc acc aac act cat att atg gct act gag gca tct   5671
386    Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala Thr Glu Ala Ser
387           1865              1870              1875
388    aat tac gcc cag tat cgg gtt gtt cgg gct acg att cgt tat cgc ccg   5719
389    Asn Tyr Ala Gln Tyr Arg Val Val Arg Ala Thr Ile Arg Tyr Arg Pro
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390          1880            1885            1890            1895
391     ttg gtg cca aat gct gtt ggt ggt tat gct atc tct att tct ttc tgg   5767
392     Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser Ile Ser Phe Trp
393                  1900            1905            1910
394     cct caa act aca act acc cct act tct gtt gac atg aat tct atc act   5815
395     Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met Asn Ser Ile Thr
396             1915            1920            1925
397     tct act gat gtc agg atc ttg gtc cag ccc ggt ata gcc tcc gag tta   5863
398     Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile Ala Ser Glu Leu
399          1930            1935            1940
400     gtc atc cct agt gaa cgc ctt cac tac cgc aac caa ggc tgg cgc tct   5911
401     Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln Gly Trp Arg Ser
402          1945            1950            1955
403     gtt gag acc acg ggt gtg gcc gaa gag gag gct acc tcc ggt ctg gta   5959
404     Val Glu Thr Thr Gly Val Ala Glu Glu Glu Ala Thr Ser Gly Leu Val
405          1960            1965            1970            1975
406     atg ctt tgt att cat ggc tcc cct gtt aac tcc tac act aat aca cct   6007
407     Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr Thr Asn Thr Pro
408                  1980            1985            1990
409     tac acc ggt gca ttg ggg ctt ctt gat ttt gca tta gaa ctt gaa ttt   6055
410     Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu Glu Leu Glu Phe
411             1995            2000            2005
412     aga aat ttg aca ccc ggg aac act aac acc cgt gtt tcc cgg tat act   6103
413     Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val Ser Arg Tyr Thr
414             2010            2015            2020
415     agc aca gcc cgc cac cgg ctg cgc cgc ggt gct gat ggg acc gct gag   6151
416     Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp Gly Thr Ala Glu
417             2025            2030            2035
418     ctc acc acc aca gca gcc aca cgc ttc atg aag gat ttg cat ttt act   6199
419     Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp Leu His Phe Thr
420     2040            2045            2050            2055
421     ggt acg aac ggc gtt ggt gag gtg ggt cgt ggt att gcc ctg act ctg   6247
422     Gly Thr Asn Gly Val Gly Glu Val Gly Arg Gly Ile Ala Leu Thr Leu
423                  2060            2065            2070
424     ttt aat ctt gct gat acg ctt ctt ggt ggt tta ccg aca gaa ttg att   6295
425     Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile
426             2075            2080            2085
427     tcg tcg gct ggg ggt caa ctg ttt tac tcc cgc cct gtt gtc tcg gcc   6343
428     Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala
429             2090            2095            2100
430     aat ggc gag cca aca gta aag tta tac aca tct gtt gag aat gcg cag   6391
431     Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln
432             2105            2110            2115
433     caa gac aag ggc atc acc att cca cac gac ata gat tta ggt gac tcc   6439
434     Gln Asp Lys Gly Ile Thr Ile Pro His Asp Ile Asp Leu Gly Asp Ser
435     2120            2125            2130            2135
436     cgt gtg gtt atc cag gat tat gat aac cag cac gaa caa gat cga cct   6487
437     Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp Arg Pro
438             2140            2145            2150
439     acc ccg tca cct gcc ccc tcc cgc cct ttc tca gtt ctt cgt gcc aat   6535
```

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440          Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu Arg Ala Asn
441                  2155              2160                  2165
442          gat gtt ttg tgg ctc tct ctc act gcc gct gag tac grc cag acc acg    6583
443          Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr Xaa Gln Thr Thr
444                  2170              2175                  2180
445          tat ggg tcg tcc acc aac cct atg tat gtc tct gat aca gtc acg ctt    6631
446          Tyr Gly Ser Ser Thr Asn Pro Met Tyr Val Ser Asp Thr Val Thr Leu
447                  2185              2190                  2195
448          gtt aat gta gcc act ggt gct cag gct gtt gcc cgc tct ctt gac tgg    6679
449          Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg Ser Leu Asp Trp
450          2200              2205              2210                  2215
451          tct aaa gtt act ctg gat ggt cgc cct ctt act acc att cag cag tat    6727
452          Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Thr Thr Ile Gln Gln Tyr
453                  2220              2225                  2230
454          tct aag aaa ttt tat gtt ctc ccg ctt cgs ggg aag ctg tcc ttt tgg    6775
455          Ser Lys Lys Phe Tyr Val Leu Pro Leu Xaa Gly Lys Leu Ser Phe Trp
456                  2235              2240                  2245
457          gag gct ggt acg acc aag gcc ggc tac ccg tat aat tat aat acc act    6823
458          Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr
459                  2250              2255                  2260
460          gct agt gac caa att ttg att gag aac gcg gcc ggt cac cgt gtc gcc    6871
461          Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala Gly His Arg Val Ala
462                  2265              2270                  2275
463          att tct act tat acc act agt ttg ggt gcc ggc cct acc tcg aty tct    6919
464          Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro Thr Ser Xaa Ser
465          2280              2285              2290                  2295
466          gcg gtc ggt gta cta gct cca cat tcg gcc ctt gct gtt ctc gag gat    6967
467          Ala Val Gly Val Leu Ala Pro His Ser Ala Leu Ala Val Leu Glu Asp
468                  2300              2305                  2310
469          act gtt gat tat cct gct cgt gcc cat act ttt gat gat ttc tgc ccg    7015
470          Thr Val Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro
471                  2315              2320                  2325
472          gag tgt cgc acc ctt ggt ctg cag ggt tgt gca ttc caa tct act att    7063
473          Glu Cys Arg Thr Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Ile
474                  2330              2335                  2340
475          gct gaa ctt cag cgt ctt aaa atg aag gta ggt aaa acc cgg gag tct    7111
476          Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Ser
477                  2345              2350                  2355
478          taa ttaattcctt ttgtgccccc ttcgcagttc tctttggctt tatttctcat    7164
479          2360  delete
480          ttctgctttc cgcgctccct ggaaaaaaaa aaaaaaaa                           7202
```

E-->

```
481      <210> 92
482      <211> 660
483      <212> PRT
484      <213> Hepatitis E virus
485      <400> 92  ← please ensure Xlet amino acids start directly under <400> 92 (as submitted
486          Met Arg Pro Arg Ala Val Leu Leu Leu Phe Leu Met Phe            file, they
487          1          5                  10                                did not)
488          Leu Pro Met Leu Pro Ala Pro Pro Ala Gly Gln Pro Ser Gly Arg Arg
```

please ensure these amino acid numbers are properly aligned — do not use TAB codes between nos

```
      489    15              20              25
      490    Arg Gly Arg Arg Ser Gly Gly Ala Gly Gly Gly Phe Trp Ser Asp Arg
      491    30              35              40              45
      492    Val Asp Ser Gln Pro Phe Ala Leu Pro Tyr Ile His Pro Thr Asn Pro
      493    50              55              60
      494    Phe Ala Ala Asp Val Val Ser Gln Pro Gly Ala Gly Thr Arg Pro Arg
E-->  495    65              70              75
      496    Gln Pro Pro Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ser Lys Arg
E-->  497    80              85              90
      498    Pro Ser Val Ala Pro Arg Arg Arg Ser Thr Pro Ala Gly Ala Ala Pro
E-->  499    95              100             105
      500    Leu Thr Ala Ile Ser Pro Ala Pro Asp Thr Ala Pro Val Pro Asp Val
      501    110             115             120             125
      502    Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser
      503    130             135             140
      504    Pro Leu Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala
      505    145             150             155
      506    Ala Pro Leu Asn Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His
      507    160             165             170
      508    Ile Met Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Val Arg
      509    175             180             185
      510    Ala Thr Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr
      511    90              195             200             205
      512    Ala Ile Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser
      513    210             215             220
      514    Val Asp Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln
      515    225             230             235
      516    Pro Gly Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr
      517    240             245             250
      518    Arg Asn Gln Gly Trp Arg Ser Val Glu Thr Thr Gly Val Ala Glu Glu
      519    255             260             265
      520    Glu Ala Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val
      521    70              275             280             285
      522    Asn Ser Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp
      523    290             295             300
      524    Phe Ala Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn
      525    305             310             315
      526    Thr Arg Val Ser Arg Tyr Thr Ser Thr Ala Arg His Arg Leu Arg Arg
      527    320             325             330
      528    Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe
      529    335             340             345
      530    Met Lys Asp Leu His Phe Thr Gly Thr Asn Gly Val Gly Glu Val Gly
      531    50              355             360             365
      532    Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly
      533    370             375             380
      534    Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr
      535    385             390             395
      536    Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr
      537    400             405             410
      538    Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Thr Ile Pro His
```

add 1

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           539      415                420                425
           540      Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn
           541      30                 435                440                445
           542      Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro
           543           450                455                460
           544      Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala
           545      465                470                475
W-->       546      Ala Glu Tyr Xaa Gln Thr Thr Tyr Gly Ser Ser Thr Asn Pro Met Tyr
           547      480                485                490
           548      Val Ser Asp Thr Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala
           549      495                500                505
           550      Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro
           551      10                 515                520                525
           552      Leu Thr Thr Ile Gln Gln Tyr Ser Lys Lys Phe Tyr Val Leu Pro Leu
           553           530                535                540
W-->       554      Xaa Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr
           555      545                550                555
           556      Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn
           557      560                565                570
           558      Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly
           559      575                580                585
W-->       560      Ala Gly Pro Thr Ser Xaa Ser Ala Val Gly Val Leu Ala Pro His Ser
           561      90                 595                600                605
           562      Ala Leu Ala Val Leu Glu Asp Thr Val Asp Tyr Pro Ala Arg Ala His
           563           610                615                620
           564      Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Thr Leu Gly Leu Gln Gly
           565      625                630                635
           566      Cys Ala Phe Gln Ser Thr Ile Ala Glu Leu Gln Arg Leu Lys Met Lys
           567      640                645                650
           568      Val Gly Lys Thr Arg Glu Ser
           569      655                660
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/468,147**

Input Set: **I468147.RAW**

Line	?	Error/Warning	Original Text
479	E	Number of Bases conflict w/ Running Total	2360
495	E	Invalid/Missing Amino Acid Numbering	65 70
497	E	Invalid/Missing Amino Acid Numbering	80 85 9
499	E	Invalid/Missing Amino Acid Numbering	95 100 10
546	W	"N" or "Xaa" used: Feature required	Ala Glu Tyr Xaa Gln Thr Thr Tyr Gly Ser S
554	W	"N" or "Xaa" used: Feature required	Xaa Gly Lys Leu Ser Phe Trp Glu Ala Gly T
560	W	"N" or "Xaa" used: Feature required	Ala Gly Pro Thr Ser Xaa Ser Ala Val Gly V